



SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Quertermous, Thomas
Hogan, Brigid
Snodgrass, H. Ralph
Zupancic, Thomas J.
- (ii) TITLE OF INVENTION: DEVELOPMENTALLY-REGULATED ENDOTHELIAL
CELL LOCUS-1
- (iii) NUMBER OF SEQUENCES: 29
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Pennie & Edmonds
 - (B) STREET: 1155 Avenue of the Americas
 - (C) CITY: New York
 - (D) STATE: New York
 - (E) COUNTRY: United States
 - (F) ZIP: 10036-2711
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: To Be Assigned
 - (B) FILING DATE: 05-JUN-1996
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Poissant, Brian M.
 - (B) REGISTRATION NUMBER: 28,462
 - (C) REFERENCE/DOCKET NUMBER: 8907-034
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (212) 790-9090
 - (B) TELEFAX: (212) 869-8864/9741
 - (C) TELEX: 66141 Pennie

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 85 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Asp Leu Leu Val Pro Thr Lys Val Thr Gly Ile Ile Thr Gln Gly Xaa
1 5 10 15

Xaa Ala Lys Asp Phe Gly Asp Val Leu Phe Val Gly Ser Tyr Lys Leu
 20 25 30
 Ala Tyr Ser Asn Asp Gly Glu His Trp Met Val His Gln Asp Glu Lys
 35 40 45
 Gln Arg Lys Asp Lys Val Phe Gln Gly Asn Phe Asp Asn Asp Thr His
 50 55 60
 Arg Lys Asn Val Ile Asp Pro Pro Ile Tyr Ala Arg Phe Ile Arg Ile
 65 70 75 80
 Leu Pro Leu Xaa Xaa
 85

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 85 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Asp Leu Gly Ser Ser Lys Glu Val Thr Gly Ile Ile Thr Gln Gly Xaa
 1 5 10 15
 Xaa Ala Arg Asn Phe Gly Ser Val Gln Phe Val Ala Ser Tyr Lys Val
 20 25 30
 Ala Tyr Ser Asn Asp Ser Ala Asn Trp Thr Glu Tyr Gln Asp Pro Arg
 35 40 45
 Thr Gly Ser Ser Lys Val Phe Gln Gly Asn Leu Asp Asn Asn Ser His
 50 55 60
 Lys Lys Asn Ile Phe Glu Lys Pro Phe Met Ala Arg Tyr Val Arg Val
 65 70 75 80
 Leu Pro Val Xaa Xaa
 85

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 85 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Asp Leu Leu Lys Ile Lys Lys Ile Thr Ala Ile Ile Thr Gln Gly Xaa
 1 5 10 15
 Xaa Cys Lys Ser Leu Ser Ser Glu Met Tyr Val Lys Ser Tyr Thr Ile
 20 25 30
 His Tyr Ser Glu Gln Gly Val Glu Trp Lys Pro Tyr Arg Leu Lys Ser
 35 40 45
 Ser Met Val Asp Lys Ile Phe Glu Gly Asn Thr Asn Thr Lys Gly His
 50 55 60
 Val Lys Asn Phe Phe Asn Pro Pro Ile Ile Ser Arg Phe Ile Arg Val
 65 70 75 80
 Ile Pro Lys Xaa Xaa
 85

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 85 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Asp Leu Gln Lys Thr Met Lys Val Thr Gly Ile Ile Thr Gln Gly Xaa
 1 5 10 15
 Xaa Val Lys Ser Leu Phe Thr Ser Met Phe Val Lys Glu Phe Leu Ile
 20 25 30
 Ser Ser Ser Gln Asp Gly His His Trp Thr Xaa Xaa Gln Ile Leu Tyr
 35 40 45
 Asn Gly Lys Val Lys Val Phe Gln Gly Asn Gln Asp Ser Ser Thr Pro
 50 55 60
 Met Met Asn Ser Leu Asp Pro Pro Leu Leu Thr Arg Xaa Xaa Xaa Xaa
 65 70 75 80
 Xaa Xaa Xaa Xaa Xaa
 85

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 35 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Asp Leu Glu Asn Leu Arg Phe Val Ser Gly Ile Gly Thr Gln Gly Ala
1 5 10 15
Ile Ser Lys Glu Thr Lys Lys Lys Tyr Phe Val Lys Ser Tyr Lys Val
20 25 30
Asp Ile Ser Ser Asn Gly Glu Asp Trp Ile Xaa Xaa Thr Leu Lys Gly
35 40 45
Asp Asn Lys His Leu Val Phe Thr Gly Asn Thr Asp Ala Thr Asp Val
50 55 60
Val Tyr Arg Pro Phe Ser Lys Pro Val Ile Thr Arg Phe Val Arg Leu
65 70 75 80
Arg Pro Val Thr Trp
85

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 85 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Asp Leu Ala Glu Glu Lys Ile Val Arg Gly Val Ile Ile Gln Gly Xaa
1 5 10 15
Xaa Gly Lys His Lys Glu Asn Lys Val Phe Met Arg Lys Phe Lys Ile
20 25 30
Gly Tyr Ser Asn Asn Gly Thr Glu Trp Glu Met Ile Met Asp Ser Ser
35 40 45
Lys Asn Lys Pro Lys Thr Phe Glu Gly Asn Thr Asn Tyr Asp Thr Pro
50 55 60
Glu Leu Arg Thr Phe Xaa Ala His Ile Thr Thr Gly Phe Ile Arg Ile
65 70 75 80
Ile Pro Xaa Xaa Xaa
85

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 85 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Gly Cys Glu Val Pro Arg Thr Phe Met Cys Val Ala Leu Gln Gly Xaa
1 5 10 15
Xaa Xaa Arg Gly Xaa Asp Ala Asp Gln Trp Val Thr Ser Tyr Lys Ile
20 25 30
Arg Tyr Ser Leu Asp Asn Val Ser Trp Phe Xaa Xaa Xaa Xaa Glu
35 40 45
Tyr Arg Asn Gly Ala Ala Ile Thr Gly Val Thr Asp Arg Asn Thr Val
50 55 60
Val Asn His Phe Phe Asp Thr Pro Ile Arg Ala Arg Ser Ile Ala Ile
65 70 75 80
His Pro Leu Thr Xaa
85

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 85 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Asp Leu Xaa Xaa Xaa Xaa Val Thr Gly Ile Ile Thr Gln Gly Xaa
1 5 10 15
Xaa Xaa Lys Xaa Xaa Xaa Xaa Xaa Phe Val Xaa Ser Tyr Lys Ile
20 25 30
Xaa Tyr Ser Xaa Asp Gly Xaa Xaa Trp Xaa Xaa Xaa Xaa Xaa Xaa
35 40 45
Xaa Xaa Lys Xaa Lys Val Phe Xaa Gly Asn Thr Asp Xaa Xaa Thr Xaa
50 55 60
Xaa Xaa Asn Xaa Phe Xaa Xaa Pro Ile Xaa Xaa Arg Phe Ile Arg Xaa
65 70 75 80
Xaa Pro Xaa Xaa Xaa
85

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2303 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 619..2058

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GAATTCCGGT TAACTGAGGA CAAAGGGTAA TGCAGAAGTG ATATTTGATT TCCATTCTCA	60
TTCCAGTGG CCTTGATATT TAACTGATT CCTGCCACCA GGTCCCTGGG CCACCCTGTC	120
CCTGCGTCTC ATATTTCTGC ATGCTGCTTT GTTTGTATAT AGTGCGCTCC TGGCCTCAGG	180
CTCGCTCCCC TCCAGCTCTC GCTTCATTGT TCTCCAAGTC AGAAGCCCCC GCATCCGCCG	240
CGCAGCAGCG TGAGCCGTAG TCACTGCTGG CCGCTTCGCC TGCCTGCGCG CACGGAAATC	300
GGGGAGCCAG GAACCCAAGG AGCCGCCGTC CGCCCGCTGT GCCTCTGCTA GACCACTCGC	360
AGCCCCAGCC TCTCTCAAGC GCACCCACCT CCGCGCACCC CAGCTCAGGC GAAGCTGGAG	420
TGAGGGTGAA TCACCCTTTC TCTAGGGCCA CCACTCTTTT ATCGCCCTTC CCAAGATTTG	480
AGAAGCGCTG CGGGAGGAAA GACGTCCTCT TGATCTCTGA CAGGGCGGGG TTTACTGCTG	540
TCCTGCAGGC GCGCCTCGCC TACTGTGCCC TCCGCTACGA CCCC GGACCA GCCCAGGTCA	600
CGTCCGTGAG AAGGGATC ATG AAG CAC TTG GTA GCA GCC TGG CTT TTG GTT	651
Met Lys His Leu Val Ala Ala Trp Leu Leu Val	
1 5 10	
GGA CTC AGC CTC GGG GTG CCC CAG TTC GGC AAA GGT GAC ATT TGC AAC	699
Gly Leu Ser Leu Gly Val Pro Gln Phe Gly Lys Gly Asp Ile Cys Asn	
15 20 25	
CCG AAC CCC TGT GAA AAT GGT GGC ATC TGT CTG TCA GGA CTG GCT GAT	747
Pro Asn Pro Cys Glu Asn Gly Gly Ile Cys Leu Ser Gly Leu Ala Asp	
30 35 40	
GAT TCC TTT TCC TGT GAG TGT CCA GAA GGC TTC GCA GGT CCG AAC TGC	795
Asp Ser Phe Ser Cys Glu Cys Pro Glu Gly Phe Ala Gly Pro Asn Cys	
45 50 55	
TCT AGT GTT GTG GAG GTT GCA TCA GAT GAA GAA AAG CCT ACT TCA GCA	843
Ser Ser Val Val Glu Val Ala Ser Asp Glu Glu Lys Pro Thr Ser Ala	
60 65 70 75	
GGT CCC TGC ATC CCT AAC CCA TGC CAT AAC GGA GGA ACC TGT GAG ATA	891
Gly Pro Cys Ile Pro Asn Pro Cys His Asn Gly Gly Thr Cys Glu Ile	
80 85 90	
AGC GAA GCC TAT CGA GGA GAC ACA TTC ATA GGC TAT GTT TGT AAA TGT	939
Ser Glu Ala Tyr Arg Gly Asp Thr Phe Ile Gly Tyr Val Cys Lys Cys	
95 100 105	
CCT CGG GGA TTT AAT GGG ATT CAC TGT CAG CAC AAT ATA AAT GAA TGT	987
Pro Arg Gly Phe Asn Gly Ile His Cys Gln His Asn Ile Asn Glu Cys	
110 115 120	
GAA GCT GAG CCT TGC AGA AAT GGC GGA ATA TGT ACC GAC CTT GTT GCT	1035

Glu	Ala	Glu	Pro	Cys	Arg	Asn	Gly	Gly	Ile	Cys	Thr	Asp	Leu	Val	Ala			
125						130				135								
AAC	TAC	TCT	TGT	GAA	TGC	CCA	GGA	GAA	TTT	ATG	GGA	CGA	AAT	TGT	CAA		1083	
Asn	Tyr	Ser	Cys	Glu	Cys	Pro	Gly	Glu	Phe	Met	Gly	Arg	Asn	Cys	Gln			
140					145					150					155			
TAT	AAA	TGC	TCT	GGG	CAC	TTG	GGA	ATC	GAA	GGT	GGG	ATC	ATA	TCT	AAT		1131	
Tyr	Lys	Cys	Ser	Gly	His	Leu	Gly	Ile	Glu	Gly	Gly	Ile	Ile	Ser	Asn			
				160					165					170				
CAG	CAA	ATC	ACA	GCT	TCA	TCT	AAT	CAC	CGA	GCT	CTT	TTT	GGA	CTC	CAG		1179	
Gln	Gln	Ile	Thr	Ala	Ser	Ser	Asn	His	Arg	Ala	Leu	Phe	Gly	Leu	Gln			
			175					180					185					
AAG	TGG	TAT	CCC	TAC	TAT	GCT	CGA	CTT	AAT	AAG	AAG	GGC	CTT	ATA	AAT		1227	
Lys	Trp		Pro	Tyr	Tyr	Ala	Arg	Leu	Asn	Lys	Lys	Gly	Leu	Ile	Asn			
		190					195					200						
GCC	TGG	ACA	GCT	GCT	GAA	AAT	GAC	AGA	TGG	CCA	TGG	ATT	CAG	ATA	AAT		1275	
Ala	Trp	Thr	Ala	Ala	Glu	Asn	Asp	Arg	Trp	Pro	Trp	Ile	Gln	Ile	Asn			
	205					210					215							
TTG	CAA	AGA	AAA	ATG	AGA	GTC	ACT	GGT	GTT	ATT	ACC	CAA	GGA	GCA	AAA		1323	
Leu	Gln	Arg	Lys	Met	Arg	Val	Thr	Gly	Val	Ile	Thr	Gln	Gly	Ala	Lys			
220					225					230					235			
AGG	ATT	GGA	AGC	CCA	GAG	TAC	ATA	AAA	TCC	TAC	AAA	ATT	GCC	TAC	AGC		1371	
Arg	Ile	Gly	Ser	Pro	Glu	Tyr	Ile	Lys	Ser	Tyr	Lys	Ile	Ala	Tyr	Ser			
				240					245					250				
AAT	GAC	GGG	AAG	ACC	TGG	GCA	ATG	TAC	AAA	GTA	AAA	GGC	ACC	AAT	GAA		1419	
Asn	Asp	Gly	Lys	Thr	Trp	Ala	Met	Tyr	Lys	Val	Lys	Gly	Thr	Asn	Glu			
			255					260					265					
GAG	ATG	GTC	TTT	CGT	GGA	AAT	GTT	GAT	AAC	AAC	ACA	CCA	TAT	GCT	AAT		1467	
Glu	Met	Val	Phe	Arg	Gly	Asn	Val	Asp	Asn	Asn	Thr	Pro	Tyr	Ala	Asn			
		270					275					280						
TCT	TTC	ACA	CCC	CCA	ATC	AAA	GCT	CAG	TAT	GTA	AGA	CTC	TAC	CCC	CAA		1515	
Ser	Phe	Thr	Pro	Pro	Ile	Lys	Ala	Gln	Tyr	Val	Arg	Leu	Tyr	Pro	Gln			
	285					290					295							
ATT	TGT	CGA	AGG	CAT	TGT	ACT	TTA	AGA	ATG	GAA	CTT	CTT	GGC	TGT	GAG		1563	
Ile	Cys	Arg	Arg	His	Cys	Thr	Leu	Arg	Met	Glu	Leu	Leu	Gly	Cys	Glu			
300					305					310					315			
CTC	TCA	GGC	TGT	TCA	GAA	CCT	TTG	GGG	ATG	AAA	TCA	GGG	CAT	ATA	CAA		1611	
Leu	Ser	Gly	Cys	Ser	Glu	Pro	Leu	Gly	Met	Lys	Ser	Gly	His	Ile	Gln			
				320					325					330				
GAC	TAC	CAG	ATC	ACT	GCC	TCC	AGC	GTC	TTC	AGA	ACA	CTC	AAC	ATG	GAC		1659	
Asp	Tyr	Gln	Ile	Thr	Ala	Ser	Ser	Val	Phe	Arg	Thr	Leu	Asn	Met	Asp			
				335				340					345					
ATG	TTT	ACT	TGG	GAA	CCA	AGG	AAA	GCC	AGG	CTG	GAC	AAG	CAA	GGC	AAA		1707	
Met	Phe	Thr	Trp	Glu	Pro	Arg	Lys	Ala	Arg	Leu	Asp	Lys	Gln	Gly	Lys			
		350					355					360						
GTA	AAT	GCC	TGG	ACT	TCC	GGC	CAT	AAC	GAC	CAG	TCA	CAA	TGG	TTA	CAG		1755	
Val	Asn	Ala	Trp	Thr	Ser	Gly	His	Asn	Asp	Gln	Ser	Gln	Trp	Leu	Gln			
	365					370					375							

GTT GAT CTT CTT GTC CCT ACT AAG GTG ACA GGC ATC ATT ACA CAA GGA Val Asp Leu Leu Val Pro Thr Lys Val Thr Gly Ile Ile Thr Gln Gly 380 385 390 395	1803
GCT AAA GAT TTT GGT CAC GTG CAG TTT GTT GGG TCA TAC AAA CTA GCT Ala Lys Asp Phe Gly His Val Gln Phe Val Gly Ser Tyr Lys Leu Ala 400 405 410	1851
TAC AGC AAT GAT GGA GAA CAC TGG ATG GTG CAC CAG GAT GAA AAA CAG Tyr Ser Asn Asp Gly Glu His Trp Met Val His Gln Asp Glu Lys Gln 415 420 425	1899
AGG AAA GAC AAG GTT TTT CAA GGC AAT TTT GAC AAT GAC ACT CAC AGG Arg Lys Asp Lys Val Phe Gln Gly Asn Phe Asp Asn Asp Thr His Arg 430 435 440	1947
AAA AAT GTC ATC GAC CCT CCC ATC TAT GCA CGA TTC ATA AGA ATC CTT Lys Asn Val Ile Asp Pro Pro Ile Tyr Ala Arg Phe Ile Arg Ile Leu 445 450 455	1995
CCT TGG TCC TGG TAT GGA AGG ATC ACT CTG CGG TCA GAG CTG CTG GGC Pro Trp Ser Trp Tyr Gly Arg Ile Thr Leu Arg Ser Glu Leu Leu Gly 460 465 470 475	2043
TGC GCA GAG GAG GAA TGAAGTGC GGCCGCACAT CCCACAATGC TTTTCTTTAT Cys Ala Glu Glu Glu 480	2098
TTTCCTATAA GATCTCCAC GAAATGAACT GTGTGAAGCT GATGGAACT GCATTTGTTT	2158
TTTTCAAAGT GTTCAAATTA TGGTAGGCTA CTGACTGTCT TTTTAGGAGT TCTAAGCTTG	2218
CCTTTTAAAT AATTTAATTT GGTTCCTTT GCTCAACTCT CTTATGTAAT ATCACACTGT	2278
CTGTGAGTTA CTCTTCTTGT TCTCT	2303

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 480 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Lys His Leu Val Ala Ala Trp Leu Leu Val Gly Leu Ser Leu Gly 1 5 10 15
Val Pro Gln Phe Gly Lys Gly Asp Ile Cys Asn Pro Asn Pro Cys Glu 20 25 30
Asn Gly Gly Ile Cys Leu Ser Gly Leu Ala Asp Asp Ser Phe Ser Cys 35 40 45
Glu Cys Pro Glu Gly Phe Ala Gly Pro Asn Cys Ser Ser Val Val Glu 50 55 60
Val Ala Ser Asp Glu Glu Lys Pro Thr Ser Ala Gly Pro Cys Ile Pro 65 70 75 80

Asn Pro Cys His Asn Gly Gly Thr Cys Glu Ile Ser Glu Ala Tyr Arg
 85 90 95
 Gly Asp Thr Phe Ile Gly Tyr Val Cys Lys Cys Pro Arg Gly Phe Asn
 100 105 110
 Gly Ile His Cys Gln His Asn Ile Asn Glu Cys Glu Ala Glu Pro Cys
 115 120 125
 Arg Asn Gly Gly Ile Cys Thr Asp Leu Val Ala Asn Tyr Ser Cys Glu
 130 135 140
 Cys Pro Gly Glu Phe Met Gly Arg Asn Cys Gln Tyr Lys Cys Ser Gly
 145 150 155 160
 His Leu Gly Ile Glu Gly Gly Ile Ile Ser Asn Gln Gln Ile Thr Ala
 165 170 175
 Ser Ser Asn His Arg Ala Leu Phe Gly Leu Gln Lys Trp Tyr Pro Tyr
 180 185 190
 Tyr Ala Arg Leu Asn Lys Lys Gly Leu Ile Asn Ala Trp Thr Ala Ala
 195 200 205
 Glu Asn Asp Arg Trp Pro Trp Ile Gln Ile Asn Leu Gln Arg Lys Met
 210 215 220
 Arg Val Thr Gly Val Ile Thr Gln Gly Ala Lys Arg Ile Gly Ser Pro
 225 230 235 240
 Glu Tyr Ile Lys Ser Tyr Lys Ile Ala Tyr Ser Asn Asp Gly Lys Thr
 245 250 255
 Trp Ala Met Tyr Lys Val Lys Gly Thr Asn Glu Glu Met Val Phe Arg
 260 265 270
 Gly Asn Val Asp Asn Asn Thr Pro Tyr Ala Asn Ser Phe Thr Pro Pro
 275 280 285
 Ile Lys Ala Gln Tyr Val Arg Leu Tyr Pro Gln Ile Cys Arg Arg His
 290 295 300
 Cys Thr Leu Arg Met Glu Leu Leu Gly Cys Glu Leu Ser Gly Cys Ser
 305 310 315 320
 Glu Pro Leu Gly Met Lys Ser Gly His Ile Gln Asp Tyr Gln Ile Thr
 325 330 335
 Ala Ser Ser Val Phe Arg Thr Leu Asn Met Asp Met Phe Thr Trp Glu
 340 345 350
 Pro Arg Lys Ala Arg Leu Asp Lys Gln Gly Lys Val Asn Ala Trp Thr
 355 360 365
 Ser Gly His Asn Asp Gln Ser Gln Trp Leu Gln Val Asp Leu Leu Val
 370 375 380
 Pro Thr Lys Val Thr Gly Ile Ile Thr Gln Gly Ala Lys Asp Phe Gly
 385 390 395 400
 His Val Gln Phe Val Gly Ser Tyr Lys Leu Ala Tyr Ser Asn Asp Gly
 405 410 415

Glu His Trp Met Val His Gln Asp Glu Lys Gln Arg Lys Asp Lys Val
420 425 430
Phe Gln Gly Asn Phe Asp Asn Asp Thr His Arg Lys Asn Val Ile Asp
435 440 445
Pro Pro Ile Tyr Ala Arg Phe Ile Arg Ile Leu Pro Trp Ser Trp Tyr
450 455 460
Gly Arg Ile Thr Leu Arg Ser Glu Leu Leu Gly Cys Ala Glu Glu Glu
465 470 475 480

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1780 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..1779

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TCT CTT TAG TCA CCA CTC TCG CCC TCT CCA AGA ATT TGT TTA ACA AAG Ser Leu * Ser Pro Leu Ser Pro Ser Pro Arg Ile Cys Leu Thr Lys 1 5 10 15	48
CGC TGA GGA AAG AGA ACG TCT TCT TGA ATT CTT TAG TAG GGG CGG AGT Arg * Gly Lys Arg Thr Ser Ser * Ile Leu * * Gly Arg Ser 20 25 30	96
CTG CTG CTG CCC TGC GCT GCC ACC TCG GCT ACA CTG CCC TCC GCG ACG Leu Leu Leu Pro Cys Ala Ala Thr Ser Ala Thr Leu Pro Ser Ala Thr 35 40 45	144
ACC CCT GAC CAG CCG GGG TCA CGT CCG GGA GAC GGG ATC ATG AAG CGC Thr Pro Asp Gln Pro Gly Ser Arg Pro Gly Asp Gly Ile Met Lys Arg 50 55 60	192
TCG GTA GCC GTC TGG CTC TTG GTC GGG CTC AGC CTC GGT GTC CCC CAG Ser Val Ala Val Trp Leu Leu Val Gly Leu Ser Leu Gly Val Pro Gln 65 70 75 80	240
TTC GGC AAA GGT GAT ATT TGT GAT CCC AAT CCA TGT GAA AAT GGA GGT Phe Gly Lys Gly Asp Ile Cys Asp Pro Asn Pro Cys Glu Asn Gly Gly 85 90 95	288
ATC TGT TTG CCA GGA TTG GCT GTA GGT TCC TTT TCC TGT GAG TGT CCA Ile Cys Leu Pro Gly Leu Ala Val Gly Ser Phe Ser Cys Glu Cys Pro 100 105 110	336
GAT GGC TTC ACA GAC CCC AAC TGT TCT AGT GTT GTG GAG GTT GCA TCA Asp Gly Phe Thr Asp Pro Asn Cys Ser Ser Val Val Glu Val Ala Ser 115 120 125	384

GAT GAA GAA GAA CCA ACT TCA GCA GGT CCC TGC ACT CCT AAT CCA TGC Asp Glu Glu Glu Pro Thr Ser Ala Gly Pro Cys Thr Pro Asn Pro Cys 130 135 140	432
CAT AAT GGA GGA ACC TGT GAA ATA AGT GAA GCA TAC CGA GGG GAT ACA His Asn Gly Gly Thr Cys Glu Ile Ser Glu Ala Tyr Arg Gly Asp Thr 145 150 155 160	480
TTC ATA GGC TAT GTT TGT AAA TGT CCC CGA GGA TTT AAT GGG ATT CAC Phe Ile Gly Tyr Val Cys Lys Cys Pro Arg Gly Phe Asn Gly Ile His 165 170 175	528
TGT CAG CAC AAC ATA AAT GAA TGC GAA GTT GAG CCT TGC AAA AAT GGT Cys Gln His Asn Ile Asn Glu Cys Glu Val Glu Pro Cys Lys Asn Gly 180 185 190	576
GGA ATA TGT ACA GAT CTT GTT GCT AAC TAT TCC TGT GAG TGC CCA GGC Gly Ile Cys Thr Asp Leu Val Ala Asn Tyr Ser Cys Glu Cys Pro Gly 195 200 205	624
GAA TTT ATG GGA AGA AAT TGT CAA TAC AAA TGC TCA GGC CCA CTG GGA Glu Phe Met Gly Arg Asn Cys Gln Tyr Lys Cys Ser Gly Pro Leu Gly 210 215 220	672
ATT GAA GGT GGA ATT ATA TCA AAC CAG CAA ATC ACA GCT TCC TCT ACT Ile Glu Gly Gly Ile Ile Ser Asn Gln Gln Ile Thr Ala Ser Ser Thr 225 230 235 240	720
CAC CGA GCT CTT TTT GGA CTC CAA AAA TGG TAT CCC TAC TAT GCA CGT His Arg Ala Leu Phe Gly Leu Gln Lys Trp Tyr Pro Tyr Tyr Ala Arg 245 250 255	768
CTT AAT AAG AAG GGG CTT ATA AAT GCG TGG ACA GCT GCA GAA AAT GAC Leu Asn Lys Lys Gly Leu Ile Asn Ala Trp Thr Ala Ala Glu Asn Asp 260 265 270	816
AGA TGG AAG CGG TGG ATT CAG ATA AAT TTG CAA AGA AAA ATG AGA GTT Arg Trp Lys Arg Trp Ile Gln Ile Asn Leu Gln Arg Lys Met Arg Val 275 280 285	864
ACT GGT GTG ATT ACC CAA GGG GCC AAG AGG ATT GGA AGC CCA GAG TAT Thr Gly Val Ile Thr Gln Gly Ala Lys Arg Ile Gly Ser Pro Glu Tyr 290 295 300	912
ATA AAA TTC TAC AAA ATT GCC TAC AGT AAT GAT GGA AAG ACT TGG GCA Ile Lys Phe Tyr Lys Ile Ala Tyr Ser Asn Asp Gly Lys Thr Trp Ala 305 310 315 320	960
ATG TAC AAA GTG AAA GGC ACC AAT GAA GAC ATG GTG TTT CGT GGA AAC Met Tyr Lys Val Lys Gly Thr Asn Glu Asp Met Val Phe Arg Gly Asn 325 330 335	1008
ATT GAT AAC AAC ACT CCA TAT GCT AAC TCT TTC ACA CCC CCC ATA AAA Ile Asp Asn Asn Thr Pro Tyr Ala Asn Ser Phe Thr Pro Pro Ile Lys 340 345 350	1056
GCT CAG TAT GTA AGA CTC TAT CCC CAA GTT TGT CGA AGA CAT TGC ACT Ala Gln Tyr Val Arg Leu Tyr Pro Gln Val Cys Arg Arg His Cys Thr 355 360 365	1104
TTG CGA ATG GAA CTT CTT GGC TGT GAA CTG TCG GGT TGT TCT GAG CCT Leu Arg Met Glu Leu Leu Gly Cys Glu Leu Ser Gly Cys Ser Glu Pro 370 375 380	1152

CTG GGT ATG AAA TCA GGA CAT ATA CAA GAC TAT CAG ATC ACT GCC TCC Leu Gly Met Lys Ser Gly His Ile Gln Asp Tyr Gln Ile Thr Ala Ser 385 390 395 400	1200
AGC ATC TTC AGA ACG CTC AAC ATG GAC ATG TTC ACT TGG GAA CCA AGG Ser Ile Phe Arg Thr Leu Asn Met Asp Met Phe Thr Trp Glu Pro Arg 405 410 415	1248
AAA GCT CGG CTG GAC AAG CAA GGC AAA GTG AAT GCC TGG ACC TCT GGC Lys Ala Arg Leu Asp Lys Gln Gly Lys Val Asn Ala Trp Thr Ser Gly 420 425 430	1296
CAC AAT GAC CAG TCA CAA TGG TTA CAG GTG GAT CTT CTT GTT CCA ACC His Asn Asp Gln Ser Gln Trp Leu Gln Val Asp Leu Leu Val Pro Thr 435 440 445	1344
AAA GTG ACT GGC ATC ATT ACA CAA GGA GCT AAA GAT TTT GGT CAT GTA Lys Val Thr Gly Ile Ile Gln Gly Ala Lys Asp Phe Gly His Val 450 455 460	1392
CAG TTT GTT GGC TCC TAC AAA CTG GCT TAC AGC AAT GAT GGA GAA CAC Gln Phe Val Gly Ser Tyr Lys Leu Ala Tyr Ser Asn Asp Gly Glu His 465 470 475 480	1440
TGG ACT GTA TAC CAG GAT GAA AAG CAA AGA AAA GAT AAG GTT TTC CAG Trp Thr Val Tyr Gln Asp Glu Lys Gln Arg Lys Asp Lys Val Phe Gln 485 490 495	1488
GGA AAT TTT GAC AAT GAC ACT CAC AGA AAA AAT GTC ATC GAC CCT CCC Gly Asn Phe Asp Asn Asp Thr His Arg Lys Asn Val Ile Asp Pro Pro 500 505 510	1536
ATC TAT GCA CGA CAC ATA AGA ATC CTT CCT TGG TCC TGG TAC GGG AGG Ile Tyr Ala Arg His Ile Arg Ile Leu Pro Trp Ser Trp Tyr Gly Arg 515 520 525	1584
ATC ACA TTG GCG TCA GAG CTG CTG GGC TGC ACA GAG GAG GAA TGA GGG Ile Thr Leu Ala Ser Glu Leu Leu Gly Cys Thr Glu Glu Glu * Gly 530 535 540	1632
GAG GCT ACA TTT CAC AAC CGT CTT CCC TAT TTG GGT AAA AGT ATC TCC Glu Ala Thr Phe His Asn Arg Leu Pro Tyr Leu Gly Lys Ser Ile Ser 545 550 555 560	1680
ATG GAA TGA ACT GTG TAA AAT CTG TAG GAA ACT GAA TGG TTT TTT TTT Met Glu * Thr Val * Asn Leu * Glu Thr Glu Trp Phe Phe Phe 565 570 575	1728
TTT TCA TGA AAA AGT GGT CAA ATT ATG GTA GGC AAC TAA CGG TGT TTT Phe Ser * Lys Ser Gly Gln Ile Met Val Gly Asn * Arg Cys Phe 580 585 590	1776
TAC C Tyr	1780

(2). INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Ser Leu * Ser Pro Leu Ser Pro Ser Pro Arg Ile Cys Leu Thr Lys
1 5 10 15

Arg

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Gly Lys Arg Thr Ser Ser
1 5

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 517 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Ile Leu * * Gly Arg Ser Leu Leu Leu Pro Cys Ala Ala Thr Ser
1 5 10 15

Ala Thr Leu Pro Ser Ala Thr Thr Pro Asp Gln Pro Gly Ser Arg Pro
20 25 30

Gly Asp Gly Ile Met Lys Arg Ser Val Ala Val Trp Leu Val Gly
35 40 45

Leu Ser Leu Gly Val Pro Gln Phe Gly Lys Gly Asp Ile Cys Asp Pro
50 55 60

Asn Pro Cys Glu Asn Gly Gly Ile Cys Leu Pro Gly Leu Ala Val Gly
65 70 75 80

Ser Phe Ser Cys Glu Cys Pro Asp Gly Phe Thr Asp Pro Asn Cys Ser
85 90 95

Ser Val Val Glu Val Ala Ser Asp Glu Glu Glu Pro Thr Ser Ala Gly
100 105 110

Pro Cys Thr Pro Asn Pro Cys His Asn Gly Gly Thr Cys Glu Ile Ser
115 120 125

Glu Ala Tyr Arg Gly Asp Thr Phe Ile Gly Tyr Val Cys Lys Cys Pro
130 135 140

Arg Gly Phe Asn Gly Ile His Cys Gln His Asn Ile Asn Glu Cys Glu
145 150 155 160

Val Glu Pro Cys Lys Asn Gly Gly Ile Cys Thr Asp Leu Val Ala Asn
 165 170 175
 Tyr Ser Cys Glu Cys Pro Gly Glu Phe Met Gly Arg Asn Cys Gln Tyr
 180 185 190
 Lys Cys Ser Gly Pro Leu Gly Ile Glu Gly Gly Ile Ile Ser Asn Gln
 195 200 205
 Gln Ile Thr Ala Ser Ser Thr His Arg Ala Leu Phe Gly Leu Gln Lys
 210 215 220
 Trp Tyr Pro Tyr Tyr Ala Arg Leu Asn Lys Lys Gly Leu Ile Asn Ala
 225 230 235 240
 Trp Thr Ala Ala Glu Asn Asp Arg Trp Lys Arg Trp Ile Gln Ile Asn
 245 250 255
 Leu Gln Arg Lys Met Arg Val Thr Gly Val Ile Thr Gln Gly Ala Lys
 260 265 270
 Arg Ile Gly Ser Pro Glu Tyr Ile Lys Phe Tyr Lys Ile Ala Tyr Ser
 275 280 285
 Asn Asp Gly Lys Thr Trp Ala Met Tyr Lys Val Lys Gly Thr Asn Glu
 290 295 300
 Asp Met Val Phe Arg Gly Asn Ile Asp Asn Asn Thr Pro Tyr Ala Asn
 305 310 315 320
 Ser Phe Thr Pro Pro Ile Lys Ala Gln Tyr Val Arg Leu Tyr Pro Gln
 325 330 335
 Val Cys Arg Arg His Cys Thr Leu Arg Met Glu Leu Leu Gly Cys Glu
 340 345 350
 Leu Ser Gly Cys Ser Glu Pro Leu Gly Met Lys Ser Gly His Ile Gln
 355 360 365
 Asp Tyr Gln Ile Thr Ala Ser Ser Ile Phe Arg Thr Leu Asn Met Asp
 370 375 380
 Met Phe Thr Trp Glu Pro Arg Lys Ala Arg Leu Asp Lys Gln Gly Lys
 385 390 395 400
 Val Asn Ala Trp Thr Ser Gly His Asn Asp Gln Ser Gln Trp Leu Gln
 405 410 415
 Val Asp Leu Leu Val Pro Thr Lys Val Thr Gly Ile Ile Thr Gln Gly
 420 425 430
 Ala Lys Asp Phe Gly His Val Gln Phe Val Gly Ser Tyr Lys Leu Ala
 435 440 445
 Tyr Ser Asn Asp Gly Glu His Trp Thr Val Tyr Gln Asp Glu Lys Gln
 450 455 460
 Arg Lys Asp Lys Val Phe Gln Gly Asn Phe Asp Asn Asp Thr His Arg
 465 470 475 480
 Lys Asn Val Ile Asp Pro Pro Ile Tyr Ala Arg His Ile Arg Ile Leu
 485 490 495

Pro Trp Ser Trp Tyr Gly Arg Ile Thr Leu Ala Ser Glu Leu⁵¹⁰ Leu Gly
500 505

Cys Thr Glu Glu Glu
515

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Gly Glu Ala Thr Phe His Asn Arg Leu Pro Tyr Leu Gly Lys Ser Ile
1 5 10 15

Ser Met Glu * Thr Val * Asn Leu
20 25

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Glu Thr Glu Trp Phe Phe Phe Ser
1 5

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Lys Ser Gly Gln Ile Met Val Gly Asn
1 5

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Arg Cys Phe Tyr
1

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 318 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GACAGATGGC CATGGATTCA GATAAATTTG CAAAGAAAAA TGAGAGTCAC TGGTGTATT	60
ACCCAAGGAG CAAAAGGAT TGGAAGCCCA GAGTACATAA AATCCTACAA AATGCCTAC	120
AGCAATGACG GGAAGACCTG GGCAATGTAC AAAGTAAAAG GCACCAATGA AGAGATGGTC	180
TTTCGTGGAA ATGTTGATAA CAACACACCA TATGCTAATT CTTTCACACC CCCAATCAAA	240
GCTCAGTATG TAAGACTCTA CCCCCAAATT TGTCGAAGGC ATTGTACTTT AAGAATGGAA	300
CTTCTTGGCT GTGAGCTC	318

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 320 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Cys Ser Thr Gln Leu Gly Met Glu Gly Gly Ala Ile Ala Asp Ser Gln	1	5	10	15
Ile Ser Ala Ser Tyr Val Tyr Met Gly Phe Met Gly Leu Gln Arg Trp	20	25	30	
Gly Pro Glu Leu Ala Arg Leu Tyr Arg Thr Gly Ile Val Asn Ala Trp	35	40	45	
His Ala Ser Asn Tyr Asp Xaa Ser Lys Pro Trp Ile Gln Val Asn Leu	50	55	60	
Leu Arg Lys Met Arg Val Ser Gly Val Met Thr Gln Gly Ala Ser Arg	65	70	75	80
Ala Gly Arg Ala Glu Tyr Leu Lys Thr Phe Lys Val Ala Tyr Ser Leu	85	90	95	

Asp Gly Xaa Arg Lys Phe Glu Phe Ile Gln Asp Glu Ser Gly Gly Asp
 100 105 110
 Lys Glu Phe Leu Gly Asn Leu Asp Asn Asn Ser Leu Lys Val Asn Met
 115 120 125
 Phe Asn Pro Thr Leu Glu Ala Gln Tyr Ile Arg Leu Tyr Pro Val Ser
 130 135 140
 Cys His Arg Gly Cys Thr Leu Arg Phe Glu Leu Leu Gly Cys Glu Leu
 145 150 155 160
 His Gly Cys Leu Glu Pro Leu Gly Leu Lys Asn Asn Thr Ile Pro Asp
 165 170 175
 Ser Gln Met Ser Ala Ser Ser Ser Tyr Lys Thr Trp Asn Leu Arg Ala
 180 185 190
 Phe Gly Trp Tyr Pro His Leu Gly Arg Leu Asp Asn Gln Gly Lys Ile
 195 200 205
 Asn Ala Trp Thr Ala Gln Ser Asn Ser Ala Lys Glu Trp Leu Gln Val
 210 215 220
 Asp Leu Gly Thr Gln Arg Gln Val Thr Gly Ile Ile Thr Gln Gly Ala
 225 230 235 240
 Arg Asp Phe Gly His Ile Gln Tyr Val Glu Ser Tyr Lys Val Ala His
 245 250 255
 Ser Asp Asp Gly Val Gln Trp Thr Val Tyr Xaa Xaa Glu Glu Gln Gly
 260 265 270
 Ser Ser Lys Val Phe Gln Gly Asn Leu Asp Asn Asn Ser His Lys Lys
 275 280 285
 Asn Ile Phe Glu Lys Pro Phe Met Ala Arg Tyr Val Arg Val Leu Pro
 290 295 300
 Val Ser Trp His Asn Arg Ile Thr Leu Arg Leu Glu Leu Leu Gly Cys
 305 310 315 320

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 321 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Cys Ser Gly Pro Leu Gly Ile Glu Gly Gly Ile Ile Ser Asn Gln Gln
 1 5 10 15
 Ile Thr Ala Ser Ser Thr His Arg Ala Leu Phe Gly Leu Gln Lys Trp
 20 25 30

Tyr Pro Tyr Tyr Ala Arg Leu Asn Lys Lys Gly Leu Ile Asn Ala Trp
 35 40 45
 Thr Ala Ala Glu Asn Asp Arg Trp Asn Arg Trp Ile Gln Ile Asn Leu
 50 55 60
 Gln Arg Lys Met Arg Val Thr Gly Val Ile Thr Gln Gly Ala Lys Arg
 65 70 75 80
 Ile Gly Ser Pro Glu Tyr Ile Lys Phe Tyr Lys Ile Ala Tyr Ser Asn
 85 90 95
 Asp Gly Lys Thr Trp Ala Met Tyr Lys Val Lys Gly Thr Asn Glu Asp
 100 105 110
 Met Val Phe Arg Gly Asn Ile Asp Asn Asn Thr Pro Tyr Ala Asn Ser
 115 120 125
 Phe Thr Pro Pro Ile Lys Ala Gln Tyr Val Arg Leu Tyr Pro Gln Val
 130 135 140
 Cys Arg Arg His Cys Thr Leu Arg Met Glu Leu Leu Gly Cys Glu Leu
 145 150 155 160
 Ser Gly Cys Ser Glu Pro Leu Gly Met Lys Ser Gly His Ile Gln Asp
 165 170 175
 Tyr Gln Ile Thr Ala Ser Ser Ile Phe Arg Thr Leu Asn Met Asp Met
 180 185 190
 Phe Thr Trp Glu Pro Arg Lys Ala Arg Leu Asp Lys Gln Gly Lys Val
 195 200 205
 Asn Ala Trp Thr Ser Gly His Asn Asp Gln Ser Gln Trp Leu Gln Val
 210 215 220
 Xaa Leu Leu Val Pro Thr Lys Val Thr Gly Ile Ile Thr Gln Gly Ala
 225 230 235 240
 Lys Asp Xaa Gly His Val Gln Phe Val Gly Ser Tyr Lys Leu Ala Tyr
 245 250 255
 Ser Asn Asp Gly Glu His Trp Thr Val Xaa Gln Asp Glu Lys Gln Arg
 260 265 270
 Lys Asp Lys Val Xaa Gln Gly Asn Phe Asp Asn Asp Thr His Arg Lys
 275 280 285
 Asn Val Ile Asp Pro Pro Ile Tyr Ala Arg His Ile Arg Ile Leu Pro
 290 295 300
 Trp Ser Trp Tyr Gly Arg Ile Thr Leu Ala Ser Glu Leu Leu Gly Cys
 305 310 315 320
 Thr

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 25 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:

(D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Met Lys Arg Ser Val Ala Val Trp Leu Leu Val Gly Leu Ser Leu Gly
1 5 10 15
Val Pro Gln Phe Gly Lys Gly Asp Ile
20 25

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Cys Asp Pro Asn Pro Cys Glu Asn Gly Gly Ile Cys Leu Pro Gly Leu
1 5 10 15
Ala Val Gly Xaa Xaa Xaa Xaa Ser Phe Ser Cys Glu Cys Pro Asp
20 25 30
Gly Phe Thr Asp Pro Asn Cys Ser Ser Val Val Glu Val Ala Ser Asp
35 40 45
Glu Glu Glu Pro Thr Ser Ala Gly Pro
50 55

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Cys Thr Pro Asn Pro Cys His Asn Gly Gly Thr Cys Glu Ile Ser Glu
1 5 10 15
Ala Tyr Arg Gly Asp Thr Phe Ile Gly Tyr Val Cys Lys Cys Pro Arg
20 25 30

Gly Phe Asn Gly Ile His Cys Gln His Asn Ile
35 40

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Cys Glu Val Glu Pro Cys Lys Asn Gly Gly Ile Cys Thr Asp Leu Val
1 5 10 15
Ala Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asn Tyr Ser Cys Glu Cys Pro Gly
20 25 30
Glu Phe Met Gly Arg Asn Cys Gln Tyr Lys
35 40

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Cys Xaa Xaa Xaa Pro Cys Xaa Asn Gly Gly Xaa Cys Xaa Xaa Xaa Xaa
1 5 10 15
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Tyr Xaa Cys Xaa Cys Xaa Xaa
20 25 30
Gly Tyr Xaa Gly Xaa Xaa Cys Xaa
35 40

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 310 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1..309

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

NGTGATATTT GTGATCCCAA TCCATGTGAA AATGGAGGTA TCTGTTTGCC AGGATTGGCT	60
GTAGGTTTCCT TTTCTGTGA GTGTCCAGAT GGCTTCACAG ACCCCAACTG TTCTAGTGTT	120
GTGGAGGTTG GTCCCTGCAC TCCTAATCCA TGCCATAATG GAGGAACCTG TGAAATAAGT	180
GAAGCATACC GAGGGGATAC ATTCATAGGC TATGTTTGTA AATGTCCCCG AGGATTTAAT	240
GGGATTCACT GTCAGCACAA CATAAATGAA TGCGAAGTTG AGCCTTGCAA AAATGGTGGA	300
ATATGTACAG	310

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2308 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 549..1211

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GAATTCGGG AGGGAGGGTA GGGGGGCGGG CCGCGGGGG CCAAAGCCAG CTAGGCTCAG	60
TCTCACACGC GCGCCGCCAC TGTTTGATA TAGTGCGCTC CTGGCCTCAG GCTCGCTCCC	120
CTCCAGCTCT CGCTTCATTG TTCTCCAAGT CAGAAGCCCC CGCATCCGCC GCGCAGCAGC	180
GTGAGCCGTA GTCACGTCTG GCCGCTTCGC CTGCGTGCGC GCACGGAAAT CGGGGAGCCA	240
GGAACCCAAG GAGCCGCCGT CCGCCCGCTG TGCCTCTGCT AGACCACTCG CAGCCCCAGC	300
CTCTCTCAAG CGCACCCACC TCCGCGCACC CCAGCTCAGG CGAAGCTGGA GTGAGGGTGA	360
ATCACCCTTT CTCTAGGGCC ACCACTCTTT TATCGCCCTT CCAAGATTT GAGAAGCGCT	420
GCGGGAGGAA AGACGTCCTC TTGATCTCTG ACAGGGCGGG GTTTACTGCT GTCCTGCAGG	480
CGCGCCTCGC CTA CTGTGCTG CTCCGCTACG ACCCCGGACC AGCCCAGGTC ACGTCCGTGA	540
GAAGGGATCA TGAAGCACTT GGTAGCAGCC TGGCTTTTGG TTGGACTCAG CCTCGGGGTG	600
CCCCAGTTCG GCAAAGGTGA CATTTGCAAC CCGAACCCTT GTGAAAATGG TGGCATCTGT	660
CTGTCAGGAC TGGCTGATGA TTCCTTTTCC TGTGAGTGTC CAGAAGGCTT CGCAGGTCCC	720
AACTGCTCTA GTGTTGTGGA GGTGTCATCA GATGAAGAAA AGCCTACTTC AGCAGGTCCC	780
TGCATCCCTA ACCCATGCCA TAACGGAGGA ACCTGTGAGA TAAGCGAAGC CTATCGAGGA	840

GACACATTCA TAGGCTATGT TTGTAAATGT CCTCGGGGAT TTAATGGGAT TCACTCTCAG	900
CACAATATAA ATGAATGTGA AGCTGAGCCT TGCAGAAATG GCGGAATATG TACCGACCTT	960
GTTGCTAACT ACTCTTGTGA ATGCCCAGGA GAATTTATGG GACGAAATG TCAATATAAA	1020
TGCTCTGGGC ACTTGGGAAT CGAAGGTGGG ATCATATCTA ATCAGCAAAT CACAGCTTCA	1080
TCTAATCACC GAGCTCTTTT TGGACTCCAG AAGTGGTATC CCTACTATGC TAGACTTAAT	1140
AAGAAGGGCC TTATAAATGC CTGGACAGCT GCTGAAAATG ACAGATGGCC ATGGATTGAG	1200
GTAACAGTGG GATGAGACAA ATCCATTTCC CAAATTATCA GAATCATTAT AGAAGTAGGT	1260
TAGGGAGAAT TGGCTGTGAT TCTTTCTCAT GGTTAAAATG TGATTAGTT CAGAATTAAC	1320
ATGGTTGGAA ACTCTAAAAA ATGTGGAAAA CAGGAACATT CTATGTCTGA AAATCTGAAA	1380
ATAGCATCAA GATGAAAAA TTCTTTAGTC ATAAATATAC TCTTTAAGT TATAGTAGAG	1440
AAAAAGATCT TATCATTTCA TAAGTGGACT TTTGGGATAG CATTGGAAAT GTAAATGAAA	1500
TAAATACCTA ATTGAAAAA GTTTATTCTA AAGTGTTAAT ATTTAGCAAC AGATTGAGAG	1560
ACAAGAAAGT AACAATTCAA TCTGTGTATT TTTGTGAGA AATAGTTTCC CATGTGCAA	1620
TATAAAGTGC GCATCATATC ATGATAATAT CCAACTGTCT GCAGAACTCC CTTTCATAAA	1680
TGAGAGAATT TTAATTCATA GTGCCTTATA TCCTCATCAG CCATCTGACT TTAATACAGA	1740
AGAAAACAAT GAAATGATGC ATTAAGTGCT TTGCTAGAAG AAACATCATA GCAAAGCTGA	1800
TAGCCACAT TCTGTGCANN NAAGCTTCCA GAGCACTCGA GAAAAAGCAG AAATGAGATG	1860
TTTTATGAAA ACCGAAAAGA TAATCTGATT TCTGTGAAAT ATACTTTTGA TCATGTGGTT	1920
CTTTAAGATA GTCATAACA AGTCATTACT AGCAGATACC AAATGGGAGA AAATTTCCAG	1980
TATACTGAGG GTCAAGGCAG TCATGCTGAA ACTACATGAG GTCAGGAAG TTTTGAAATA	2040
AGGTGATTTT GGAAGGATAC CTTCAACTGG CCTAGATTTT CAAGAAACAG TGTAATCAAC	2100
AGCCAAACAT GAGAATCTAG CTAACAGCAT TTAGAAAACC AGAACTAAGA GTGTTACTGG	2160
GGAATTGCAT TTAAATCCAG TATGAGAGTT TGCAAATGCC GTATTCTTCT AAGGGGTTTG	2220
TGCCACATTT TGTTACCATG GAGTCCTCTG TAAGAACTTT ATTAGATAAA TCATCTTTAC	2280
ACTATAATTT GAATAAAAGC CGGAATTC	2308

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 480 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Met	Lys	Arg	Ser	Val	Ala	Val	Trp	Leu	Leu	Val	Gly	Leu	Ser	Leu	Gly
1					5				10					15	

Val Pro Gln Phe Gly Lys Gly Asp Ile Cys Asp Pro Asn Pro Cys Glu
 20 25 30
 Asn Gly Gly Ile Cys Leu Pro Gly Leu Ala Val Gly Ser Phe Ser Cys
 35 40 45
 Glu Cys Pro Asp Gly Phe Thr Asp Pro Asn Cys Ser Ser Val Val Glu
 50 55 60
 Val Ala Ser Asp Glu Glu Glu Pro Thr Ser Ala Gly Pro Cys Thr Pro
 65 70 75 80
 Asn Pro Cys His Asn Gly Gly Thr Cys Glu Ile Ser Glu Ala Tyr Arg
 85 90 95
 Gly Asp Thr Phe Ile Gly Tyr Val Cys Lys Cys Pro Arg Gly Phe Asn
 100 105 110
 Gly Ile His Cys Gln His Asn Ile Asn Glu Cys Glu Val Glu Pro Cys
 115 120 125
 Lys Asn Gly Gly Ile Cys Thr Asp Leu Val Ala Asn Tyr Ser Cys Glu
 130 135 140
 Cys Pro Gly Glu Phe Met Gly Arg Asn Cys Gln Tyr Lys Cys Ser Gly
 145 150 155 160
 Pro Leu Gly Ile Glu Gly Gly Ile Ile Ser Asn Gln Gln Ile Thr Ala
 165 170 175
 Ser Ser Thr His Arg Ala Leu Phe Gly Leu Gln Lys Trp Tyr Pro Tyr
 180 185 190
 Tyr Ala Arg Leu Asn Lys Lys Gly Leu Ile Asn Ala Trp Thr Ala Ala
 195 200 205
 Glu Asn Asp Arg Trp Lys Arg Trp Ile Gln Ile Asn Leu Gln Arg Lys
 210 215 220
 Met Arg Val Thr Gly Val Ile Thr Gln Gly Ala Lys Arg Ile Gly Ser
 225 230 235 240
 Pro Glu Tyr Ile Lys Phe Tyr Lys Ile Ala Tyr Ser Asn Asp Gly Lys
 245 250 255
 Thr Trp Ala Met Tyr Lys Val Lys Gly Thr Asn Glu Asp Met Val Phe
 260 265 270
 Arg Gly Asn Ile Asp Asn Asn Thr Pro Tyr Ala Asn Ser Phe Thr Pro
 275 280 285
 Pro Ile Lys Ala Gln Tyr Val Arg Leu Tyr Pro Gln Val Cys Arg Arg
 290 295 300
 His Cys Thr Leu Arg Met Glu Leu Leu Gly Cys Glu Leu Ser Gly Cys
 305 310 315 320
 Ser Glu Pro Leu Gly Met Lys Ser Gly His Ile Gln Asp Tyr Gln Ile
 325 330 335
 Thr Ala Ser Ser Ile Phe Arg Thr Leu Asn Met Asp Met Phe Thr Trp
 340 345 350

Glu Pro Arg Lys Ala Arg Leu Asp Lys Gln Gly Lys Val Asn Ala Trp
 355 360 365
 Thr Ser Gly His Asn Asp Gln Ser Gln Trp Leu Gln Val Xaa Leu Leu
 370 375 380
 Val Pro Thr Lys Val Thr Gly Ile Ile Thr Gln Gly Ala Lys Asp Xaa
 385 390 395 400
 Gly His Val Gln Phe Val Gly Ser Tyr Lys Leu Ala Tyr Ser Asn Asp
 405 410 415
 Gly Glu His Trp Thr Val Xaa Gln Asp Glu Lys Gln Arg Lys Asp Lys
 420 425 430
 Val Xaa Gln Gly Asn Phe Asp Asn Asp Thr His Arg Lys Asn Val Ile
 435 440 445
 Asp Pro Pro Ile Tyr Ala Arg His Ile Arg Ile Leu Pro Trp Ser Trp
 450 455 460
 Tyr Gly Arg Ile Thr Leu Ala Ser Glu Leu Leu Gly Cys Thr Glu Glu
 465 470 475
 Glu
 480